



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/030,537

DATE: 02/08/2002

TIME: 10:41:56

Input Set : A:\SeqList.txt

Output Set: N:\CRF3\02082002\J030537.raw

PS

C-11> 11 <140> CURRENT APPLICATION NUMBER: US/10/030,537

C-11> 11 <141> CURRENT FILING DATE: 2002-01-11

11 <150> PRIOR APPLICATION NUMBER: US 60/142,981

12 <151> PRIOR FILING DATE: 1999-07-12

14 <160> NUMBER OF SEQ ID NOS: 34

16 <210> SEQ ID NO: 1

17 <211> LENGTH: 1358

18 <212> TYPE: DNA

19 <213> ORGANISM: Glycine max

21 <220> FEATURE:

22 <221> NAME/KEY: CDS

23 <222> LOCATION: (24)...(1100)

25 <400> SEQUENCE: 1

ENTERED

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27 gaattcggct cgagtttgaa cca atg aca atg ctt cag aaa atg gct gag ctt      53
28                               Met Thr Met Leu Gln Lys Met Ala Glu Leu
29                               1           5           10
31 atg gag tac tct tac ctg tta gat atg gcg gac aag act gag gat cca      101
32 Met Glu Tyr Ser Tyr Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro
33                               15           20           25
35 tac atg aga cta gta tat gct tca tca ttc ttt ata tct gtc tac tat      149
36 Tyr Met Arg Leu Val Tyr Ala Ser Ser Phe Phe Ile Ser Val Tyr Tyr
37                               30           35           40
39 gcc tat caa cga acg tgg aag cca ttc aat cca att ctt ggt gag act      197
40 Ala Tyr Gln Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr
41                               45           50           55
43 tat gaa atg gtt aac cat ggt ggc att aca ttt ata tca gag cag gtc      245
44 Tyr Glu Met Val Asn His Gly Gly Ile Thr Phe Ile Ser Glu Gln Val
45                               60           65           70
47 agt cat cac cct cca atg agt gct ggg cat gct gaa act gaa cat ttc      293
48 Ser His His Pro Pro Met Ser Ala Gly His Ala Glu Thr Glu His Phe
49 75                               80           85           90
51 act tat gat gtt aca tca aaa ttg aaa acc aaa ttt ctc ggc aac tca      341
52 Thr Tyr Asp Val Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser
53                               95           100          105
55 gtt gat gta tat cct gtt gga aga acg cgt gtt acc ctc aaa aga gat      389
56 Val Asp Val Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp
57                               110          115          120

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10030537.042302

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59 ggt gtg gtc ctt gat ttg gtg cct cct cct aca aaa gtt agc aac ttg      437
60 Gly Val Val Leu Asp Leu Val Pro Pro Pro Thr Lys Val Ser Asn Leu
61      125      130      135
63 att ttt gga cga act tgg att gat tca cca gga gag atg atc ctg aca      485
64 Ile Phe Gly Arg Thr Trp Ile Asp Ser Pro Gly Glu Met Ile Leu Thr
65      140      145      150
67 aat ctg act aca ggg gac aaa gtg gtg ctg tat ttt caa cca tgt ggc      533
68 Asn Leu Thr Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly
69 155      160      165      170
71 tgg ttt gga tat gaa gtg gat ggg tac gtg tat aat tct gct gac gag      581
72 Trp Phe Gly Tyr Glu Val Asp Gly Tyr Val Tyr Asn Ser Ala Asp Glu
73      175      180      185
75 cct aag ata ctg atg act gga aaa tgg aat gag gct atg aat tat caa      629
76 Pro Lys Ile Leu Met Thr Gly Lys Trp Asn Glu Ala Met Asn Tyr Gln
77      190      195      200
79 gtt tgt gac tca gag gga gaa cca ctt cca ggc act gag ttg aaa gag      677
80 Val Cys Asp Ser Glu Gly Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu
81      205      210      215
83 att tgg aga gtt gct gat acc ccg aag aag gac aag ttc cag tac acg      725
84 Ile Trp Arg Val Ala Asp Thr Pro Lys Lys Asp Lys Phe Gln Tyr Thr
85      220      225      230
87 cat ttt gca cac aag att aac agc ttt gac act gct ccc aag aag ttg      773
88 His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu
89 235      240      245      250
91 ttg gca tct gac tct cgt cta cgt cct gat aga atg gcc ctt gag aag      821
92 Leu Ala Ser Asp Ser Arg Leu Arg Pro Asp Arg Met Ala Leu Glu Lys
93      255      260      265
95 ggt gac cta tcc aca tct ggt tat gag aag agc agt ttg gag gag agg      869
96 Gly Asp Leu Ser Thr Ser Gly Tyr Glu Lys Ser Ser Leu Glu Glu Arg
97      270      275      280
99 caa aga gct gag aag aga aac cga gag gcc aag ggc cat aag ttc act      917
100 Gln Arg Ala Glu Lys Arg Asn Arg Glu Ala Lys Gly His Lys Phe Thr
101      285      290      295
103 cct aga tgg ttt gat tta aca gat gaa gta act cct acc cct tgg ggt      965
104 Pro Arg Trp Phe Asp Leu Thr Asp Glu Val Thr Pro Thr Pro Trp Gly
105      300      305      310
107 gac ttg gaa gtt tac caa tac aac ggt aaa tat acc caa cat tgt gct      1013
108 Asp Leu Glu Val Tyr Gln Tyr Asn Gly Lys Tyr Thr Gln His Cys Ala
109 315      320      325      330
111 gcc gtt gat agt tct gag tgc att gaa gtg cct gac atc aga cca gaa      1061
112 Ala Val Asp Ser Ser Glu Cys Ile Glu Val Pro Asp Ile Arg Pro Glu
113      335      340      345
115 ttc aac cct tgg caa tat gat aat ttg gat gct gaa tag tgagcatcct      1110
116 Phe Asn Pro Trp Gln Tyr Asp Asn Leu Asp Ala Glu
117      350      355
119 tgtggaattc tttctatttt ttttaaatat cattttgtta ttaagtttgt aatgtaatct      1170
121 tgattggaat gcttgaaatt tggttttgtt ttgggtttgt tttatcactg tagtatttga      1230
123 ttaattaata gtagctatgt tagttcatca gttcactttg catggataaa tgctagtagg      1290
125 gaaattaaag ttatcttcca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaagggc      1350

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127 ggccgccc                                     1358
130 <210> SEQ ID NO: 2
131 <211> LENGTH: 1136
132 <212> TYPE: DNA
133 <213> ORGANISM: Glycine max
135 <220> FEATURE:
136 <221> NAME/KEY: CDS
137 <222> LOCATION: (73)...(975)
139 <400> SEQUENCE: 2
141 gaattcggct cgaggtcaca acttcagtgct tatggtgaat cagtgtattg cacaggttcg      60
143 gacttgctaa gc atg tgc aac aat ggt cag agt cca ctt gat agg ttc ata      111
144           Met Cys Asn Asn Gly Gln Ser Pro Leu Asp Arg Phe Ile
145           1           5           10
147 tct gtg gta gca tgg tgc ata tct acc act cgc cct gtg act ttt ggt      159
148 Ser Val Val Ala Trp Cys Ile Ser Thr Thr Arg Pro Val Thr Phe Gly
149           15           20           25
151 gtt gct cct tat aat ccc att ctt ggt gag aca cac cat gtt tca agg      207
152 Val Ala Pro Tyr Asn Pro Ile Leu Gly Glu Thr His His Val Ser Arg
153           30           35           40           45
155 gga aat ctt aat gtg tta ttg gag cag att tca cat cac cct cca gta      255
156 Gly Asn Leu Asn Val Leu Leu Glu Gln Ile Ser His His Pro Pro Val
157           50           55           60
159 act gct ctc cat gca aca gat gag aag gaa aac att gaa atg tta tgg      303
160 Thr Ala Leu His Ala Thr Asp Glu Lys Glu Asn Ile Glu Met Leu Trp
161           65           70           75
163 tgc cag cga cct gat cca aag ttt aat ggc aca tca gtt gaa gct aaa      351
164 Cys Gln Arg Pro Asp Pro Lys Phe Asn Gly Thr Ser Val Glu Ala Lys
165           80           85           90
167 gtg cat gga ata cgc cag ttg aag ctc cta aat cat ggt gaa aca tat      399
168 Val His Gly Ile Arg Gln Leu Lys Leu Leu Asn His Gly Glu Thr Tyr
169           95           100          105
171 gaa atg aat tgt cct cgc ctt tta ctt aga att ctt cca gtt cct ggt      447
172 Glu Met Asn Cys Pro Arg Leu Leu Leu Arg Ile Leu Pro Val Pro Gly
173           110          115          120          125
175 gct gat tgg gct ggt aca gtt aat ata cgg tgc cta gag aca ggt cta      495
176 Ala Asp Trp Ala Gly Thr Val Asn Ile Arg Cys Leu Glu Thr Gly Leu
177           130          135          140
179 gta gct gaa tta tcc tac aga tca agt tct ttt cta gga att ggg ggg      543
180 Val Ala Glu Leu Ser Tyr Arg Ser Ser Ser Phe Leu Gly Ile Gly Gly
181           145          150          155
183 aat cat aga gtg atc aaa ggg aag atc ctt gac tct tca tca ttg aaa      591
184 Asn His Arg Val Ile Lys Gly Lys Ile Leu Asp Ser Ser Ser Leu Lys
185           160          165          170
187 gtt cta tat gaa gtt gat ggt cat tgg gat agg acc gta aaa gtg aag      639
188 Val Leu Tyr Glu Val Asp Gly His Trp Asp Arg Thr Val Lys Val Lys
189           175          180          185
191 gac aca aat aat ggg aaa gta aga gtg ata tat gat gca aag gaa gtt      687
192 Asp Thr Asn Asn Gly Lys Val Arg Val Ile Tyr Asp Ala Lys Glu Val
193           190          195          200          205

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Input Set : A:\SeqList.txt

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195 atg tca ggt ctc gaa act cct ata ctc aag gac ata gag ggt gtg tgg      735
196 Met Ser Gly Leu Glu Thr Pro Ile Leu Lys Asp Ile Glu Gly Val Trp
197              210              215              220
199 caa aca gaa tca gct cat gtt tgg ggt gaa tta aac caa gcc att gtg      783
200 Gln Thr Glu Ser Ala His Val Trp Gly Glu Leu Asn Gln Ala Ile Val
201              225              230              235
203 agc aaa gac tgg gag aaa gca aga gaa gca aag cta aaa gtt gag gaa      831
204 Ser Lys Asp Trp Glu Lys Ala Arg Glu Ala Lys Leu Lys Val Glu Glu
205              240              245              250
207 aga caa agg gag ctt gtg aga gaa aga gaa tca aaa gga gaa aca tgg      879
208 Arg Gln Arg Glu Leu Val Arg Glu Arg Glu Ser Lys Gly Glu Thr Trp
209              255              260              265
211 att tct aag cat ttt gta gtt tct aac aac aaa gaa ggg tgg caa tgt      927
212 Ile Ser Lys His Phe Val Ser Asn Asn Lys Glu Gly Trp Gln Cys
213 270              275              280              285
215 tca cct att cat aag agt gta cct gcg gcc ccc atc aca gcc cta taa      975
216 Ser Pro Ile His Lys Ser Val Pro Ala Ala Pro Ile Thr Ala Leu
217              290              295              300
219 ttgttgtcac tgtcaagtag tgtaaagcat taaagtacat tttagaagag aatgttcata 1035
221 aaaaaattta atggttgaaa ttttgacaac aatgaagtat ataacaaaat ttaaaattag 1095
223 ttacaatttt aaaaaaaaaa aaaaaaaaaag ggcggccgcc g 1136
226 <210> SEQ ID NO: 3
227 <211> LENGTH: 1355
228 <212> TYPE: DNA
229 <213> ORGANISM: Glycine max
231 <220> FEATURE:
232 <221> NAME/KEY: CDS
233 <222> LOCATION: (32)...(1099)
235 <400> SEQUENCE: 3
237 ggaattcggc tcgaggacaa tgcttcagaa a atg gct gag ctt atg gag tac      52
238              Met Ala Glu Leu Met Glu Tyr
239              1              5
241 tct tac ctg tta gat atg gcg gac aag act gag gat cca tac atg aga      100
242 Ser Tyr Leu Leu Asp Met Ala Asp Lys Thr Glu Asp Pro Tyr Met Arg
243              10              15              20
245 cta gta tat gct tca tca ttc ttt ata tct gtc tac tat gcc tat caa      148
246 Leu Val Tyr Ala Ser Ser Phe Phe Ile Ser Val Tyr Tyr Ala Tyr Gln
247              25              30              35
249 cga acg tgg aag cca ttc aat cca att ctt ggt gag act tat gaa atg      196
250 Arg Thr Trp Lys Pro Phe Asn Pro Ile Leu Gly Glu Thr Tyr Glu Met
251 40              45              50              55
253 gtt aac cat ggt ggc att aca ttt ata tca gag cag gtc agt cat cac      244
254 Val Asn His Gly Gly Ile Thr Phe Ile Ser Glu Gln Val Ser His His
255              60              65              70
257 cct cca atg agt gct ggg cat gct gaa act gaa cat ttc act tat gat      292
258 Pro Pro Met Ser Ala Gly His Ala Glu Thr Glu His Phe Thr Tyr Asp
259              75              80              85
261 gtt aca tca aaa ttg aaa acc aaa ttt ctc ggc aac tca gtt gat gta      340
262 Val Thr Ser Lys Leu Lys Thr Lys Phe Leu Gly Asn Ser Val Asp Val

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2008-08-02 10:41:56

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TIME: 10:41:56

Input Set : A:\SeqList.txt

Output Set: N:\CRF3\02082002\J030537.raw

J030537.042302

263	90	95	100	
265	tat cct gtt gga aga acg cgt gtt acc ctc aaa aga gat ggt gtg gtc	388		
266	Tyr Pro Val Gly Arg Thr Arg Val Thr Leu Lys Arg Asp Gly Val Val			
267	105 110 115			
269	ctt gat ttg gtg cct cct cct aca aaa gtt agc aac ttg att ttt gga	436		
270	Leu Asp Leu Val Pro Pro Pro Thr Lys Val Ser Asn Leu Ile Phe Gly			
271	120 125 130 135			
273	cga act tgg att gat tca cca gga gag atg atc ctg aca aat ctg act	484		
274	Arg Thr Trp Ile Asp Ser Pro Gly Glu Met Ile Leu Thr Asn Leu Thr			
275	140 145 150			
277	aca ggg gac aaa gtg gtg ctg tat ttt caa cca tgt ggc tgg ttt gga	532		
278	Thr Gly Asp Lys Val Val Leu Tyr Phe Gln Pro Cys Gly Trp Phe Gly			
279	155 160 165			
281	gct ggt aga tat gaa gtg gat ggg tac gtg tat aat tct gct gac gag	580		
282	Ala Gly Arg Tyr Glu Val Asp Gly Tyr Val Tyr Asn Ser Ala Asp Glu			
283	170 175 180			
285	cct aag ata ctg atg act gga aaa tgg aat gag gct atg aat tat caa	628		
286	Pro Lys Ile Leu Met Thr Gly Lys Trp Asn Glu Ala Met Asn Tyr Gln			
287	185 190 195			
289	gtt tgt gac tca gag gga gaa cca ctt cca ggc act gag ttg aaa gag	676		
290	Val Cys Asp Ser Glu Gly Glu Pro Leu Pro Gly Thr Glu Leu Lys Glu			
291	200 205 210 215			
293	att tgg aga gtt gct gat acc ccg aag aag gac aag ttc cag tac acg	724		
294	Ile Trp Arg Val Ala Asp Thr Pro Lys Lys Asp Lys Phe Gln Tyr Thr			
295	220 225 230			
297	cat ttt gca cac aag att aac agc ttt gac act gct ccc aag aag ttg	772		
298	His Phe Ala His Lys Ile Asn Ser Phe Asp Thr Ala Pro Lys Lys Leu			
299	235 240 245			
301	ttg gca tct gac tct cgt cta cgt cct gat aga atg gcc ctt gag aag	820		
302	Leu Ala Ser Asp Ser Arg Leu Arg Pro Asp Arg Met Ala Leu Glu Lys			
303	250 255 260			
305	ggt gac cta tcc aca tct ggt tat gag aag agc agt ttg gag gag agg	868		
306	Gly Asp Leu Ser Thr Ser Gly Tyr Glu Lys Ser Ser Leu Glu Glu Arg			
307	265 270 275			
309	caa aga gct gag aag aga aac cga gag gcc aag ggc cat aag ttc act	916		
310	Gln Arg Ala Glu Lys Arg Asn Arg Glu Ala Lys Gly His Lys Phe Thr			
311	280 285 290 295			
313	cct aga tgg ttt gat tta aca gat gaa gta act cct acc cct tgg ggt	964		
314	Pro Arg Trp Phe Asp Leu Thr Asp Glu Val Thr Pro Thr Pro Trp Gly			
315	300 305 310			
317	gac ttg gaa gtt tac caa tac aac ggt aaa tat acc caa cat tgt gct	1012		
318	Asp Leu Glu Val Tyr Gln Tyr Asn Gly Lys Tyr Thr Gln His Cys Ala			
319	315 320 325			
321	gcc gtt gat agt tct gag tgc att gaa gtg cct gac atc aga cca gaa	1060		
322	Ala Val Asp Ser Ser Glu Cys Ile Glu Val Pro Asp Ile Arg Pro Glu			
323	330 335 340			
325	ttc aac cct tgg caa tat gat aat ttg gat gct gaa tag tgagcctcct	1109		
326	Phe Asn Pro Trp Gln Tyr Asp Asn Leu Asp Ala Glu			
327	345 350 355			

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/030,537

DATE: 02/08/2002

TIME: 10:41:57

Input Set : A:\SeqList.txt

Output Set: N:\CRF3\02082002\J030537.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:669 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:766 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:772 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13
L:789 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:799 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14
L:822 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15
L:859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
L:940 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1014 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1016 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1018 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1035 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1037 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1039 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1041 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
L:1056 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1058 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1066 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
L:1083 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1087 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1089 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1091 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1093 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:27
L:1108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1116 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1118 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1120 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1122 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:28
L:1139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1141 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29
L:1143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:29